Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application.

Listing of Claims:

1. (Previously Presented) A mutant strain of mycobacterium comprising in its genome a modified tyrosine phosphatase gene selected from *mptpA* bearing SEQ ID No. 15 and *mptpB* bearing SEQ ID NO. 16, the strain being incapable of expressing active tyrosine phosphatase.

2. (Previously Presented) A strain as claimed in claim 1, wherein the mycobacterium strain is selected from a group consisting of *M. tuberculosis* and *M. bovis.*

3. (Previously Presented) A recombinant vector comprising a modified *mptpA* gene bearing SEQ ID NO. 15.

4. (Previously Presented) A vector as claimed in claim 3, wherein the vector is pAK A.

5. (Previously Presented) A recombinant vector comprising a modified *mptpB* gene bearing SEQ ID NO. 15.

6. (Previously Presented) A recombinant vector as claimed in claim 5, wherein the vector is pBk B.

7. (Currently Amended) The ~~A~~ recombinant vector ~~as claimed in any of claims 3-6~~ of claim 3, wherein the modified *mptpA* or *mptpB* gene includes an internal region substituted with a first antibiotic resistance marker gene.

8. (Previously Presented) A recombinant vector as claimed in claim 7, wherein the antibiotic resistance marker gene imparts resistance to an antibiotic selected from hygromycin or chloramphenicol, preferably hygromycin.

9. (Currently Amended) The ~~A~~ recombinant vector ~~as claimed in any of claims 3-6~~ of claim 3, further comprising a second antibiotic marker gene inserted in its backbone.

10. (Previously Presented) A recombinant vector as claimed in claim 9, wherein the second antibiotic marker gene imparts resistance to an antibiotic selected from kanamycin or gentamycin.

11. An isolated nucleotide sequence bearing SEQ. No. 15 and representing modified *mptpA* gene.

12. An isolated nucleotide sequence SEQ. ID No. 16 and representing modified *mptpB* gene.

13. A method for developing a mutant mycobacterium strain comprising a modified tyrosine phosphatase gene in its genome, comprising the following steps:

a. extracting genomic DNA from a mycobacterium strain,

b. amplifying a tyrosine phosphatase gene alongwith flanking sequences using a primer designed from the genomic DNA of step (a) to obtain a DNA fragment,

c. characterizing the fragment of step (b) by sequencing and restriction enzymatic analysis,

d. cloning the fragment of step (b) in a non-replicative vector,

e. modifying the fragment in the non-replicative vector of step (d) by performing a step selected from insertion, deletion mutation or substitution,

f. inserting a first antibiotic resistance marker gene within the fragment of step (e) to obtain a non-replicative vector comprising a modified tyrosine phosphatase gene sleeted from *mptpA* bearing SEQ ID 15 or *mptpB* bearing SEQ ID 16,

g. cloning of a second antibiotic resistance marker gene in the backbone of the non-replicative vector of step (f), to obtain a recombinant vector,

h. introducing the recombinant vector of step (g) to obtain into a mycobacterium strain,

i. selecting for primary recombinant mycobacterium strains using the first antibiotic resistance marker gene,

j. culturing the primary recombinant mycobacterium strain of step (i) harboring the first antibiotic resistance marker gene,

k. selecting for secondary recombinant mycobacterium strains of step (j) that are sensitive to the second antibiotic resistance gene present in the vector backbone.

l. culturing the secondary recombinant mycobacterium strains of step (k), to obtain a recombinant mycobacterium strain harboring the modified tyrosine phosphatase gene which shows defective growth in activated macrophages and animals.

14. (Previously Presented) A method as claimed in claim 13, wherein the mycobacterium species is selected from a group consisting of *M. tuberculosis* and *M. bovis.*

15. (Previously Presented) A method as claimed in claim 13, wherein, the primer designed in step (b) is selected from any of SEQ ID NO: 1 to 4 for amplification of *mptpA* alongwith its flanking regions and any of SEQ ID NO: 5 to 8 for amplification of *mptpB* alongwith its flanking regions

16. (Previously Presented) A method as claimed in claim 13, wherein the tyrosine

phosphatase gene is *mptpA* gene of SEQ ID No. 11.

17. (Previously Presented) A method as claimed in claim 13, wherein the tyrosine phosphatase gene is *mptpB* gene of SEQ ID No. 12.

18. (Previously Presented) A method as claimed in claim 13, wherein step (b) the DNA fragment is a sequence bearing SEQ ID No. 13.

19. (Previously Presented) A method as claimed in claim 13, wherein in step (b) the DNA fragment is a sequence bearing SEQ ID No. 14.

20. (Previously Presented) A method as claimed in claim 13, wherein the first antibiotic resistance marker gene imparts resistance to an antibiotic selected from hygromycin or chloramphenicol, preferably hygromycin.

21. (Previously Presented) A method as claimed in claim 13, wherein the second antibiotic marker gene imparts resistance to the antibiotic kanamycin.

22. (Previously Presented) A method as claimed in claim 13, wherein the recombinant vector is pAK A.

23. (Previously Presented) A method as claimed in claim 13, wherein the recombinant vector is pBk B.

24. (Previously Presented) A method as claimed in claim 13, wherein the vector is introduced by electroporation or through phages.

25. (Previously Presented) A method as claimed in claim 13, wherein primary recombinant mycobacterium strain is selected by using an antibiotic selected from hygromycin or chloramphenicol.

26. (Previously Presented) A method as claimed in claim 13, wherein in step (k) the secondary recombinant mycobacterium strain is resistant to hygromycin or chloramphenicol but sensitive to the second antibiotic kanamycin.

27. (Previously Presented) A primer sequence adapted for amplification of *mptpA* gene selected from any of SEQ ID No. 1 to 4 alongwith its flanking regions.

28. (Previously Presented) A primer sequence adapted for amplification of *mptpB* gene selected from any of SEQ ID No. 5 to 8 alongwith its flanking regions.